

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: Portugal, Frank H.
Colwell, Rita R.
Hug, Anwarul
Chowdhury, Afzal

10 (ii) TITLE OF INVENTION: Compositions and Methods for
Differentiating Among *Shigella* Species
and *Shigella* from *E. coli* Species

15 (iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
(B) STREET: 816 Congress Avenue, Suite 1900
(C) CITY: Austin
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 78701

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not Yet Assigned
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Not Yet Assigned

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,117
(B) FILING DATE: 20-FEB-1997

40 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Norberg, Gloria L.
(B) REGISTRATION NUMBER: 36,706
(C) REFERENCE/DOCKET NUMBER: 044198.0000

45 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (512) 499-6200
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50 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60 AGAGTTTGAT CATGGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTTACCT TGTTACGACT T

21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GGCAGCAGGC CTAACACATG CAAGTCGAAC 60
GGTAACAGGA AGCAGCTTGC TGTTTCGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG 120
GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG 180
CAAGACCAAA GAGGGGGGACC TTCCGGGCCTC TTGCCATCGG ATGTGCCAG ATGGGATTAG 240
CTAGTAGGTG GGGTAACGGC TCACCTAGGC GACGATCCCT AGCTGGTCTG AGAGGATGAC 300
CAGCCACACT GGAACGTGAGA CACGGTCCAG ACTCCTACGG GAGGCAGCAG TGGGAATAT 360
TGCACAATGG GCGCAAGCCT GATGCAGCCA TGCCCGTGT ATGAAGAAGG CCTTCGGGTT 420
GTAAAGTACT TTCAGCGGGG AGGAAGGGAG TAAAGTTAAT ACCTTGCTC ATTGACGTTA 480
CCCGCAGAAG AAGCACCGGC TAACTCCGTG CCAGCAGCCG CGGTAATACG GAGGGTGCAA 540
GCGTTAATCG GAATTACTGG GCGTAAAGCG CACGCAGGCG GTTTGTTAAG TCAGATGTGA 600
ATCCCCGGG CTCAACCTGG GAACTGCATC TGATACTGGC AAGCTTGAGT CTCGTAGAGG 660
GGGGTAGAAT TCCAGGTGTA GCGGTGAAAT GCGTAAAGAT CTGGAGGAAT ACCGGTGGCG 720
AAGGCGGCCCT CCTGGACGAA GACTGACGCT CAGGTGCGAA AGCGTGGGA GAAACAGGA 780
TTAGATACCC TGGTAGTCCA CGCTGTAAAC GATGTCGACT TGGAGGTTGT GCCCTGAGG 840
TGTGGCTTCC GGAGCTAACG CGTTAAGTCG ACCGCCTGGG GAGTACGGCC GCAAGGTTAA 900
AACTCAAATG AATTGACGGG GGCCCGCACA AGCGGTGGAG CATGTGGTTT AATTCGATGC 960
AACGCGAAGA ACCTTACCTG GTCTTGACAT CCACGGAAGT TTTCAGAGAT GAGAATGTGC 1020
CTTCGGGAAC CGTGAGACAG GTGCTGCATG GCTGTCGTCA GCTCGTGTG TGAAATGTTG 1080
GGTTAAGTCC CGCAACGAGC GCAACCCTTA TCCTTTGTTG CCAGCGGTCC GGCCGGGAAC 1140
TCAAAGGAGA CTGCCAGTGA TAAACTGGAG GAAGGTGGGG ATGACGTCAA GTCATCATGG 1200
CCCTTACGAC CAGGGCTACA CACGTGCTAC AATGGCGCAT ACAAAAGAGAA GCGACCTCGC 1260

10	GAGAGCAAGC GGACCTCATA AAGTGCCTCG TAGTCCGGAT TGGAGTCTGC AACTCGACTC	1320
15	CATGAAGTCG GAATCGCTAG TAATCGTGA TCAGAAATGCC ACGGTGAATA CGTCCCCGGG	1380
20	CCTTGTACAC ACCGCCCGTC ACACCATGGG AGTGGGTTGC AAAAGAAGTA GGTAGCTTAA	1440
25	CCTTCGGGAG GGCGCTTACCA CTCTTGAT TCATGACTGG GGTGAAGTCG TAACAAGGTA	1500
30	ACCGTA	1506

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35	AGAGTTTGAT CATGGCTCAG ATTGAACGCT GGCAGCAGGC CTAACACATG CAAGTCGAAC	60
40	GGTAACAGGA AACAGCTTGC TGTTTCGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG	120
45	GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG	180
50	CAAGACCAAA GAGGGGGACC TTCCGGCCTC TTGCCATCGG ATGTGCCAG ATGGGATTAG	240
55	CTAGTAGGTG GGGTAACGGC TCACCTAGGC GACGATCCCT AGCTGGTCTG AGAGGATGAC	300
60	CAGCCACACT GGAACGTGAGA CACGGTCCAG ACTCCTACGG GAGGCAGCAG TGGGAATAT	360
65	TGCACAATGG GCGCAAGCCT GATGCAGCCA TGCCGCGTGT ATGAAGAAGG CCTTCGGGTT	420
70	GTAAAGTACT TTCAGCGGGG AGGAAGGGAG TAAAGTTAAT ACCTTTACTC ATTGACGTTA	480
75	CCCGCAGAAG AAGCACCGGC TAACTCCGTG CCAGCAGCCG CGGTAATACG GAGGGTGCAA	540
80	GCGTTAATCG GAATTACTGG GCGTAAAGCG CACGCAGGCG GTTTGTTAAG TCAGATGTGA	600
85	AATCCCCGGG CTCAACCTGG GAACTGCATC TGATACTGGC AAGCTTGAGT CTCGTAGAGG	660
90	GGGGTAGAAT TCCAGGTGTA GCGGTGAAAT GCGTAGAGAT CTGGAGGAAT ACCGGTGGCG	720
95	AAGGCGGCC CCGGACGAA GACTGACGCT CAGGTGCGAA AGCGTGGGA GCAAACAGGA	780
100	TTAGATACCC TGGTAGTCCA CGCCGTAAAC GATGTCGACT TGGAGGTTGT GCCCTTGAGG	840
105	CGTGGCTTCC GGAGCTAACG CGTTAAGTCG ACCGCCTGGG GAGTACGGCC GCAAGGTTAA	900
110	AACTCAAATG AATTGACGGG GGCCCGCACA AGCGGTGGAG CATGTGGTTT AATTGACGC	960
115	AACGCGAAGA ACTTACCTGG TCTTGACATC CACGGAACCT TCCAGAGATG GATTGGTGCC	1020
120	TTCGGGAACCT GTGAGACAGG TGCTGCATGG CTGTCGTCAG CTCGTGTTGT GAAATGTTGG	1080
125	GTAAAGTCCC GCAACGAGCG CAACCCCTAT CCTTGTTGC CAGCGGTCCG GCCGGGAAC	1140
130	CAAAGGAGAC TGCCAGTGAT AAACTGGAGG AAGGTGGGA TGACGTCAAG TCATCATGGC	1200
135	CCTTACGACC AGGGCTACAC ACGTGCTACA ATGGCGCATA CAAAGAGAAG CGACCTCGCG	1260
140	AGAGCAAGCG GACCTCATAA AGTGCCTCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC	1320

ATGAAAGTCGG	AATCGCTAGT	AATCGTGGAT	CAGAATGCCA	CGGTGAATAC	GTTCCCGGGC	1380	
CTTGTACACA	CCGCCCGTCA	CACCATGGGA	GTGGGTTGCA	AAAGAAGTAG	GTAGCTTAAC	1440	
5	CTTCGGGAGG	GCGCTTACCA	CTTTGTGATT	CATGACTGGG	GTGAAGTCGT	AACAAGGTAA	1500
	CCGTA					1505	

10 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(400, 593, 642, 737, 968, 998)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = Unknown"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25	AGAGTTTGAT	CATGGCTCAG	ATTGAACGCT	GGCGGCAGGC	CTAACACATG	CAAGTCGAAC	60
30	GGTAACAGAA	AGCAGCTTGC	TCCTTGCTG	ACGAGTGGCG	GACGGGTGAG	TAATGTCTGG	120
35	GAAACTGCCT	GATGGAGGGG	GATAACTACT	GGAAACCGTA	GCTAATACCG	CATAACGTCG	180
40	CAAGACCAAA	GAGGGGGACC	TTCGGGCCTC	TTGCCATCGG	ATGTGCCAG	ATGGGATTAG	240
45	CTAGTAGTGG	GGTAACGGCT	CACCTAGGCG	ACGATCCCTA	GCTGGTCTGA	GAGGATGACC	300
50	AGCCACACTG	GAAC TGAGAC	ACGGTCCAGA	CTCCTACGGG	AGGCAGCAGT	GGGAAATATT	360
55	GCACAATGGG	CGCAAGCCTG	ATGCAGCCAT	GCCCGTGTN	TGAANAAGGC	CTTCGGGTTG	420
60	TAAAGTACTT	TCAGCGGGGA	GGAAGGGAGT	AAAGTTAATA	CCTTTGCTCA	TTGACGTTAC	480
65	CCGCAGAAGA	AGCACCGGCT	AACTCCGTGC	CAGCAGCCGC	GGTAATACGG	AGGGTGCAAG	540
	CGTTAATCGG	AATTACTGGG	CGTAAAGCGC	ACGCAGGCGG	TTTGTAAAT	CANATGTGAA	600
	ATCCCCGGGC	TCAACCTGGG	AACTGCATCT	GATACTGGCA	ANCTTGAGTC	TCGTAGAGGG	660
	GGGTAGAATT	CCAGGTGTAG	CGGTGAAATG	CGTAGAGATC	TGGAGGAATA	CCGGTGGCGA	720
	AGGCGGCC	CTGGACNAAG	ACTGACGCTC	AGGTGCGAAA	GCGTGGGAG	CAAACAGGAT	780
	TAGATACCC	GGTAGTCCAC	GCCGTAAACG	ATGTCGACTT	GGAGGTTGTG	CCCTTGAGGC	840
	GTGGCTTCCG	GAGCTAACCG	GTAAAGTCGA	CCGCCTGGGG	AGTACGGCCG	CAAGGTTAAA	900
	ACTCAAATGA	ATTGACGGGG	GCCCCCACAA	GCGGTGGAGC	ATGTGGTTA	ATTGATGCA	960
	ACGCGAANAA	CCTTACCTGG	TCTTGACATC	CACAGAANCT	TCCAGAGATG	GATTGGTGCC	1020
	TTCGGGAAC	GTGAGACAGG	TGCTGCATGG	CTGTCGTCAG	CTCGTGTGT	GAAATGTTGG	1080
	GTAAAGTCCC	GCAACGAGCG	CAACCCTTAT	CCTTGTGTC	CAGCGGTCCG	GCCGGGAAC	1140
	CAAAGGAGAC	TGCCAGTGAT	AAACTGGAGG	AAGGTGGGGA	TGACGTCAAG	TCATCATGGC	1200

	CCTTACGACC AGGGCTACAC	ACGTGCTACA ATGGCGCATA CAAAGAGAAG CGACCTCGCG	1260
	AGAGCAAGCG GACCTCATAA	AGTGCCTCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC	1320
5	ATGAAGTCCG AATCGCTAGT	AATCGTGGAT CAGAATGTCA CGGTGAATAC GTTCCCGGGC	1380
	CTTGTACACA CCGCCCGTCA	CACCATGGGA GTGGCTTAAC CTTCGGGAGG GCGCTTACCA	1440
10	CTTTGTGATT CAT		1453

(2) INFORMATION FOR SEQ ID NO:6:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	AGAGTTTGAT CATGGCTCAG ATTGAACGCT GGCAGCAGGC CTAACACATG CAAGTCGAAC	60
	GGTAACAGGA AGCAGCTTGC TCTTCGCTGA CGAGTGGCGG ACGGGTGAGT AATGTCTGGG	120
25	AAACTGCCTG ATGGAGGGGG ATAACTACTG GAAACGGTAG CTAATACCGC ATAATGTCGC	180
	AAGACCAAAG AGGGGGACCT TCGGGCCTCT TGCCATCGGA TGTGCCAGA TGGGATTAGC	240
30	TTGTTGGTGG GTAAACGGCT CACCAAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC	300
	AGCCACATGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTG GGGAAATTG	360
	CACAATGGGC GCAAGCCTGA TGCAGCCATG CCGCGTGTAT GAAGAAGGCC TTCGGGTTGT	420
	AAAGTACTTT CAGCGGGGAG GAAGGGAGTA AAGTTAATAC CTTTGCTCAT TGACGTTACC	480
	CGCAGAAGAA GCACCGGCTA ACTCCGTGCC AGCAGCCGCG GTAATACGGA GGGTGCAAGC	540
35	GTAAATCGGA ATTACTGGC GTAAAGCGCA CGCAGGCGGT TTGTTAAGTC AGATGTGAAA	600
	TCCCCGGGCT CAACCTGGGA ACTGCATCTG ATACTGGCAA GCTTGAGTCT CGTAGAGGGG	660
40	GGTAGAATTG CAGGTGTAGC GGTGAAATGC GTAGAGATCT GGAGGAATAC CGGTGGCGAA	720
	GGCGGCCCGG TGGACGAAGA CTGACGCTCA GGTGCGAAAG CGTGGGGAGC AACAGGATT	780
	AGATAACCTG GTAGTCCACG CCGTAAACGA TGTGACTTG GAGGTTGTGC CCTTGAGGCG	840
45	TGGCTTCCGG AGCTAACGCG TTAAGTCGAC CGCCTGGGA GTACGGCCGC AAGGTTAAAA	900
	CTCAAATGAA TTGACGGGGG CCCGCACAAG CGGTGGAGCA TGTGGTTAA TTCGATGCAA	960
	CGCGAAGAAC CTTACCTGGT CTTGACATCC ACGGAAGTT TCAGAGATGA GAATGTGCCT	1020
50	TCGGGAACCG TGAGACAGGT GCTGCATGGC TGTGTCAGC TCGTGTGTG AAATGTTGGG	1080
	TTAAGTCCCG CAACGAGCGC AACCTTATC CTTTGTGCGC AGCGGTCCGG CCGGAAACTC	1140
55	AAAGGAGACT GCCAGTGATA AACTGGAGGA AGGTGGGGAT GACGTCAAGT CATCATGGCC	1200
	CTTACGACCA GGGCTACACA CGTGCTACAA TGGCGCATAC AAAGAGAAGC GACCTCGCGA	1260
60	GAGCAAGCGG ACCTCATAAA GTGCGTCCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC	1320
65		

ATGAAGTCGG	AATCGCTAGT	AATCGTGGAT	CAGAATGCCA	CGGTGAATAC	GTTCCCGGGC	1380	
CTTGCACACA	CCGCCCCGTCA	CACCATGGGA	GTGGGTTGCA	AAAGAAGTAG	GTAGCTTAAC	1440	
5	CTTCGGGAGG	GCGCTTACCA	CTTTGTGATT	CATGACTGGG	GTGAAGTCGT	AACAAGGTAA	1500
	CCGTA					1505	

10 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20	AAATTGAAGA	GTTCGATCAT	GGCTCAGATT	GAACGCTGGC	GGCAGGCCTA	ACACATGCAA	60
	GTCAACGGT	AACAGGAAGA	AGCTTGCTCT	TTGCTGACGA	GTGGCGGACG	GGTGAGTAAT	120
25	GTCTGGGAAA	CTGCCTGATG	GAGGGGGATA	ACTACTGGAA	ACGGTAGCTA	ATACCGCATA	180
	ACGTCGCAAG	ACCAAAGAGG	GGGACCTTCG	GGCCTCTTGC	CATCGGATGT	GCCCAGATGG	240
30	GATTAGCTAG	TAGGTGGGGT	AACGGCTCAC	CTAGGCGACG	ATCCCTAGCT	GGTCTGAGAG	300
	GATGACCAGC	CACACTGGAA	CTGAGACACG	GTCCAGACTC	CTACGGGAGG	CAGCAGTGGG	360
35	GAATATTGCA	CAATGGGCGC	AAGCCTGATG	CAGCCATGCC	CGCTGTATGA	AGAAGGCCTT	420
	CGGGTTGTAA	AGTACTTTCA	CGCGGGAGGA	AGGGAGTAAA	GTAAATACCT	TTGCTCATTG	480
40	ACGTTACCCG	CAGAAGAACG	ACCGGCTAAC	TCCGTGCCAG	CAGCCGCGGT	AATACGGAGG	540
	GTGCAAGCGT	TAATCGGAAT	TACTGGCGT	AAAGCGCACG	CAGGCGGTTT	GTAAAGTCAG	600
45	ATGTGAAATC	CCCAGGCTCA	ACCTGGGAAC	TGCATCTGAT	ACTGGCAAGC	TTGAGTCTCG	660
	TAGAGGGGGG	TAGAATTCCA	GGTGTAGCGG	TGAAATGCGT	AGAGATCTGG	AGGAATACCG	720
50	GTGGCGAAGG	CGGCCCCCTG	GACGAAGACT	GACGCTCAGG	TGCGAAAGCG	TGGGGAGCAA	780
	ACAGGATTAG	ATACCCCTGGT	AGTCCACGCC	GTAAACGATG	TCGACTTGGA	GGTTGTGCC	840
55	TTGAGGCCTG	GCTTCCGGAG	CTAACCGGTT	AAAGTCGACCG	CCTGGGGAGT	ACGGCCGCAA	900
	GGTTAAAACT	CAAATGAATT	GACGGGGGCC	CGCACACAAGCG	GTGGAGCATG	TGGTTAATT	960
60	CGATGCAACG	CGAAGAACCT	TACCTGGTCT	TGACATCCAC	GGAAGTTTTC	AGAGATGAGA	1020
	ATGTGCCTTC	GGGAACCGTG	AGACAGGTGC	TGCATGGCTG	TCGTCAGCTC	GTGTTGTGAA	1080
65	ATGTTGGGTT	AAGTCCCGCA	ACGAGCGCAA	CCCTTATCCT	TTGTTGCCAG	CGGTCCGGCC	1140
	GGGAACCTCAA	AGGAGACTGC	CAGTGATAAA	CTGGAGGAAG	GTGGGGATGA	CGTCAAGTCA	1200
	TCATGGCCCT	TACGACCAGG	GCTACACACG	TGCTACAATG	GCGCATACAA	AGAGAACGCA	1260
	CCTCGCGAGA	GCAAGCGGAC	CTCATAAAGT	CGCTCGTAGT	CCGGATTGGA	GTCTGCAACT	1320
	CGACTCCATG	AAGTCGGAAT	CGCTAGTAAT	CGTGGATCAG	AATGCCACGG	TGAATACGTT	1380

55 CCCGGGCCTT GTACACACCG CCCGTCACAC CATGGGAGTG GGTTGCAAAA GAAGTAGGTA 1440
56 GCTTAACCTT CGGGAGGGCG CTTACCACCT TGTGATTCAAT GACTGGGTG AAGTCGTAAC 1500
57 AAGGTAACCG TAGGGAAACC TGCGGTTGGA TCACCTCCTT A 1541

62 (2) INFORMATION FOR SEQ ID NO:8:

67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 30 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: single
71 (D) TOPOLOGY: linear

75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

80 AACAGGAAGA AGCTTGCTCT TTGCTGACGA 30

85 (2) INFORMATION FOR SEQ ID NO:9:

90 (i) SEQUENCE CHARACTERISTICS:
91 (A) LENGTH: 31 base pairs
92 (B) TYPE: nucleic acid
93 (C) STRANDEDNESS: single
94 (D) TOPOLOGY: linear

98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

103 AACAGGAAGC AGCTTGCTGT TTGCTGACG A 31

108 (2) INFORMATION FOR SEQ ID NO:10:

113 (i) SEQUENCE CHARACTERISTICS:
114 (A) LENGTH: 31 base pairs
115 (B) TYPE: nucleic acid
116 (C) STRANDEDNESS: single
117 (D) TOPOLOGY: linear

122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

127 AACAGGAAAC AGCTTGCTGT TTGCTGACG A 31

132 (2) INFORMATION FOR SEQ ID NO:11:

137 (i) SEQUENCE CHARACTERISTICS:
138 (A) LENGTH: 30 base pairs
139 (B) TYPE: nucleic acid
140 (C) STRANDEDNESS: single
141 (D) TOPOLOGY: linear

146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

151 AACAGAAAGC AGCTTGCTCT TTGCTGACGA 30

156 (2) INFORMATION FOR SEQ ID NO:12:

161 (i) SEQUENCE CHARACTERISTICS:
162 (A) LENGTH: 30 base pairs
163 (B) TYPE: nucleic acid
164 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 AACAGGAAGC AGCTTGCTCT TCGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGCAACG CGAAGAACCT TACCTGGTCT T 31

(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

30 CGACGCAACG CGAAGAACCTT ACCTGGTCTT 30

(2) INFORMATION FOR SEQ ID NO:15:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

45 GGAAGTTTTC AGAGATGAGA ATGTGCCTTC GGGAAACCGTG 40

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGAACTTTCC AGAGATGGAT TGGTGCCCTTC GGGAACTGTG 40

(2) INFORMATION FOR SEQ ID NO:17:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
65 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 AGAAGCTTCC AGAGATGGAT TGGTGCCTTC GGAACTGTG 40

(2) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGCTTGCTC TTTCGCTGACG 20

20 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAAGCAGCTT GCTCTTGCT 30 20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35 CGACGCAACG CGAAGAACTT 40 20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAAGCTTGCT TCTTGCTGA C 60 21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

65

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

SL
537
CGACGCAACG CGAAGAA

17